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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/039,659

DATE: 02/08/2002  
TIME: 08:32:59

APR 03 2002

TECH CENTER 1600/2900

Input Set : N:\Crf3\RULE60\10039659.txt  
Output Set: N:\CRF3\02082002\J039659.raw

# SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: Wang, Wei  
7 Gish, Kurt C.  
8 Schall, Thomas J.  
9 Vicari, Alain P.  
10 Zlotnik, Albert  
12 (ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS  
14 (iii) NUMBER OF SEQUENCES: 19  
16 (iv) CORRESPONDENCE ADDRESS:  
17 (A) ADDRESSEE: DNAX Research Institute  
18 (B) STREET: 901 California Avenue  
19 (C) CITY: Palo Alto  
20 (D) STATE: California  
21 (E) COUNTRY: USA  
22 (F) ZIP: 94304-1104  
24 (v) COMPUTER READABLE FORM:  
25 (A) MEDIUM TYPE: Floppy disk  
26 (B) COMPUTER: IBM PC compatible  
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
30 (vi) CURRENT APPLICATION DATA:  
C--> 31 (A) APPLICATION NUMBER: US/10/039,659  
C--> 32 (B) FILING DATE: 03-Jan-2002  
38 (C) CLASSIFICATION:  
C--> 44 (vii) PRIOR APPLICATION DATA:  
36 (A) APPLICATION NUMBER: US 08/887,977  
37 (B) FILING DATE: 03-JUL-1997  
41 (A) APPLICATION NUMBER: US 60/021,644  
42 (B) FILING DATE: 05-JUL-1996  
45 (A) APPLICATION NUMBER: US 60/028,329  
46 (B) FILING DATE: 11-OCT-1996  
48 (viii) ATTORNEY/AGENT INFORMATION:  
49 (A) NAME: Ching, Edwin P.  
50 (B) REGISTRATION NUMBER: 34,090  
51 (C) REFERENCE/DOCKET NUMBER: DX0589K1  
53 (ix) TELECOMMUNICATION INFORMATION:  
54 (A) TELEPHONE: 650-852-9192  
55 (B) TELEFAX: 650-496-1200  
58 (2) INFORMATION FOR SEQ ID NO: 1:  
60 (i) SEQUENCE CHARACTERISTICS:  
61 (A) LENGTH: 1034 base pairs  
62 (B) TYPE: nucleic acid

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63      (C) STRANDEDNESS: single
64      (D) TOPOLOGY: linear
66      (ii) MOLECULE TYPE: cDNA
69      (ix) FEATURE:
70          (A) NAME/KEY: CDS
71          (B) LOCATION: 94..525
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 AGGCTACAAG CAGGCACCAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT      60
78 TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC      114
79                                     Met Lys Leu Trp Leu Phe Ala
80                                     1             5
82 TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC      162
83 Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala
84         10             15             20
86 CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA      210
87 Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys
88     25             30             35
90 TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT      258
91 Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser
92  40             45             50             55
94 GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA      306
95 Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val
96     60             65             70
98 GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC      354
99 Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile
100     75             80             85
102 TTG ACA GCT AGG AAA AGG CTA GTC CAC TGG AAG AGC GCC TCA GAC TCT      402
103 Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser
104     90             95             100
106 CAG ACT GAA AGG AAG AAG TCA AAC CAT ATG AAG TCC AAG GTG GAG AAC      450
107 Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn
108     105             110             115
110 CCC AAC AGT ACA AGC GTG AGG AGT GCC ACC CTA GGT CAT CCC AGG ATG      498
111 Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met
112 120             125             130             135
114 GTG ATG ATG CCC AGA AAG ACC AAC AAT TAAGTTAATT ACTCAGAGTA      545
115 Val Met Met Pro Arg Lys Thr Asn Asn
116     140
118 AGCACCAGCT GGAGGATGGG CGGAGTCTGC TGAAGTGCTG TCTTCTAGGC ATGCCAGTGC      605
120 CAATGAATC ACTGAAGCTA CAGTTTCCTG TACAAGACCA GACCCACCAA CGTCTCAGCA      665
122 TGTACGAGGA AGGAATCTACT GCGCTAAAGG CCCTCCCACT CACCAAGGAG CTATTGGCTA      725
124 TTGATGATTG CTGAGGGAAG GGAGTAATTT TTTTCTCTT TCTGAAGTGT GACTTGAGTA      785
126 AATTGCCCAT AGTTCAGTAT ATAATCCCCA ACCTGTGCTC AGGCAAGCAA CCCTAATTAA      845
128 ATGCAATAGC CACATACAAA AGAAGAGGAT ATGAATAGTT TGGTAGGAGG GGCTTGTTAG      905
130 GAAGAAGACA TTAACAGGAG AGAGAGGAGC GAGAGGATAG TGAGTGTGTG AGAGTGCCTG      965
132 CACGTGTGAA ATGGTCAAAG AATTAAAAAA TAAAACTTA AAAAGCTATT AAAAAGTAAA      1025
134 AAAAATAAA      1034
137 (2) INFORMATION FOR SEQ ID NO: 2:
139      (i) SEQUENCE CHARACTERISTICS:

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140      (A) LENGTH: 144 amino acids
141      (B) TYPE: amino acid
142      (D) TOPOLOGY: linear
144      (ii) MOLECULE TYPE: protein
146      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
148 Met Lys Leu Trp Leu Phe Ala Cys Leu Val Ala Cys Phe Val Gly Ala
149   1      5      10      15
151 Trp Met Pro Val Val His Ala Gln Gly Ala Phe Glu Asp Cys Cys Leu
152      20      25      30
154 Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn
155      35      40      45
157 Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg
158      50      55      60
160 Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
161   65      70      75      80
163 Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
164      85      90      95
166 Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His
167      100     105     110
169 Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
170      115     120     125
172 Thr Leu Gly His Pro Arg Met Val Met Met Pro Arg Lys Thr Asn Asn
173      130     135     140
176 (2) INFORMATION FOR SEQ ID NO: 3:
178      (i) SEQUENCE CHARACTERISTICS:
179          (A) LENGTH: 1012 base pairs
180          (B) TYPE: nucleic acid
181          (C) STRANDEDNESS: single
182          (D) TOPOLOGY: linear
184      (ii) MOLECULE TYPE: cDNA
187      (ix) FEATURE:
188          (A) NAME/KEY: CDS
189          (B) LOCATION: 117..566
191      (ix) FEATURE:
192          (A) NAME/KEY: mat_peptide
193          (B) LOCATION: 186..566
196      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
198 TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCGGGCAT CAGCTCCCTT GACCCAGTGG      60
200 ATATCGGTGG CCCCCTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC      116
202 ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC      164
203 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
204 -23      -20      -15      -10
206 TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG      212
207 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
208      -5      1      5
210 GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT      260
211 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
212 10      15      20      25
214 TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA      308

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215 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
216                      30                      35                      40
218 TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC      356
219 Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
220                      45                      50                      55
222 AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT      404
223 Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
224                      60                      65                      70
226 TTT GCA AAG CTC CAC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT      452
227 Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
228                      75                      80                      85
230 GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG      500
231 Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
232 90                      95                      100                      105
234 TTT AGC AAT CCC ATC AGC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA      548
235 Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
236                      110                      115                      120
238 TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTTCTGGG CTCCATCGGC      596
239 Ser Ala Asn Ser Gly Leu
240                      125
242 ACAGGAGGGG CCGGATCTTT CTCCGATAAA ACCGTGCGCC TACAGACCCA GCTGTCCCCA      656
244 CGCCTCTGTC TTTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCCT CCCTCTGCAC      716
246 CCCACCAACC TCCTGCCCCG CTGGCAACTG GAAAGAAGGA GTTGGCCTGA TTTTAACCTT      776
248 TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGTAG AGAAAACCTA      836
250 GGATACCTCT CTCACCTTTCT GTTCTTTGCC GTCCACCCCG GGCCATGCCA GTGTGTCCTC      896
252 TGGGTCCCTT CCAAAAATCT GGTCAATCAA GGATCCCCTC CCAAGGCTAT GCTTTTCTAT      956
254 AACTTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAAAA AAAAAA      1012
257 (2) INFORMATION FOR SEQ ID NO: 4:
259 (i) SEQUENCE CHARACTERISTICS:
260 (A) LENGTH: 150 amino acids
261 (B) TYPE: amino acid
262 (D) TOPOLOGY: linear
264 (ii) MOLECULE TYPE: protein
266 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
268 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
269 -23 -20 -15 -10
271 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
272 -5 1 5
274 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
275 10 15 20 25
277 Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
278 30 35 40
280 Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
281 45 50 55
283 Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
284 60 65 70
286 Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
287 75 80 85
289 Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys

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290 90 95 100 105
292 Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile
293 110 115 120
295 Ser Ala Asn Ser Gly Leu
296 125
298 (2) INFORMATION FOR SEQ ID NO: 5:
300 (i) SEQUENCE CHARACTERISTICS:
301 (A) LENGTH: 801 base pairs
302 (B) TYPE: nucleic acid
303 (C) STRANDEDNESS: single
304 (D) TOPOLOGY: linear
306 (ii) MOLECULE TYPE: cDNA
309 (ix) FEATURE:
310 (A) NAME/KEY: CDS
311 (B) LOCATION: 1..288
313 (ix) FEATURE:
314 (A) NAME/KEY: mat_peptide
315 (B) LOCATION: 79..288
318 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
320 ATG TGC TGT ACC AAG AGT TTG CTC CTG GCT GCT TTG ATG TCA GTG CTG 48
321 Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu
322 -26 -25 -20 -15
324 CTA CTC CAC CTC TGC GGC GAA TCA GAA GCA GCA AGC AAC TTT GAC TGC 96
325 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
326 -10 -5 1 5
328 TGT CTT GGA TAC ACA GAC CGT ATT CTT CAT CCT AAA TTT ATT GTG GGC 144
329 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
330 10 15 20
332 TTC ACA CGG CAG CTG GCC AAT GAA GGC TGT GAC ATC AAT GCT ATC ATC 192
333 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
334 25 30 35
336 TTT CAC ACA AAG AAA AAG TTG TCT GTG TGC GCA AAT CCA AAA CAG ACT 240
337 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
338 40 45 50
340 TGG GTG AAA TAT ATT GTG CGT CTC CTC AGT AAA AAA GTC AAG AAC ATG 288
341 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
342 55 60 65 70
344 TAAAAACTGT GGCTTTTCTG GAATGGAATT GGACATAGCC CAAGAACAGA AAGAACCTTG 348
346 CTGGGGTTGG AGGTTTCACT TGCACATCAT GGAGGGTTTA GTGCTTATCT AATTGTGCC 408
348 TCACTGGACT TGTCCAATTA ATGAAGTTGA TTCATATTGC ATCATAGTTT GCTTTGTTA 468
350 AGCATCACAT TAAAGTTAAA CTGTATTTTA TGTTATTTAT AGCTGTAGGT TTTCTGTGTT 528
352 TAGCTATTTA ATACTAATTT TCCATAAGCT ATTTTGGTTT AGTGCAAAGT ATAAAAATTAT 588
354 ATTTGGGGGG GAATAAGATT ATATGGACTT TTTTGCAAGC AACAAGCTAT TTTTAAAAAA 648
356 AACTATTTA ACATTCTTTT GTTTATATTG TTTTGTCTCC TAAATTGTTG TAATTGCATT 708
358 ATAAAAATAAG AAAAATATTA ATAAGACAAA TATTGAAAAT AAAGAAACAA AAAGTTAAAA 768
360 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 801
363 (2) INFORMATION FOR SEQ ID NO: 6:
365 (i) SEQUENCE CHARACTERISTICS:
366 (A) LENGTH: 96 amino acids

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## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10039659.txt  
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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]